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(54) Method for detecting the presence of at least one single allele of a deletion mutant

(57) Method for detecting the presence of at least one single allele of a deletion mutant, specially as PCR assay for detecting the presence of at least one GSTT1*0 allele wherein a PCR is performed with two primers, of which one stems from the sequence upstream of the deletion area, and the other stems from the sequence downstream of the deletion area and wherein the production of the corresponding DNA fragment in the PCR is checked. Useful for testing of patients to check whether they are susceptible to toxins or resistant or overly sensitive to certain therapeutic agents or belonging to risk groups.

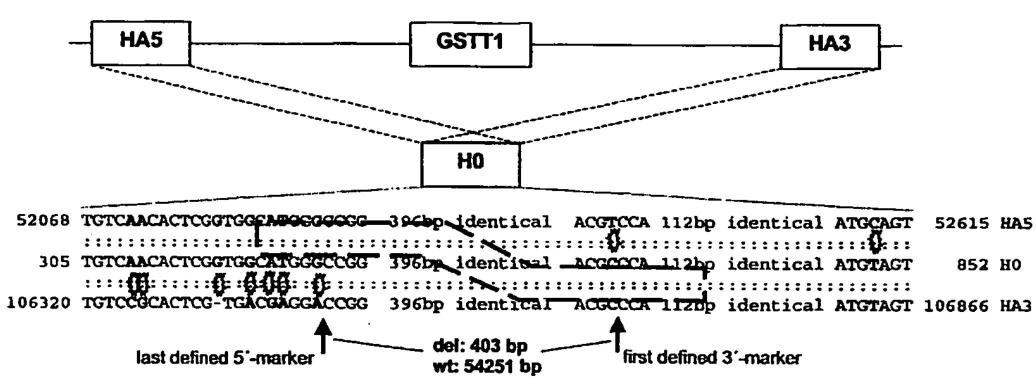

Fig. 4

EP 1 130 112 A1

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Description

[0001] This invention relates to a method for detecting the presence of at least one single allele of a deletion mutant, a PCR assay for detecting the presence of at least one GSTT1* allele and a procedure for diagnostic testing of patients to check whether they are susceptible to toxins or resistant to certain therapeutic agents or belonging to risk groups.
[0002] Human glutathione S-transferase theta (GSTT1) is an important detoxification enzyme comprising a deletion polymorphism. Approximately 20 % of Caucasians are homozygous GSTT1*0/0 failing to express any GSTT1 activity. Non conjugators may have an impaired ability to metabolically eliminate toxic compounds and may therefore be at increased risk for cancer, inflammatory diseases or chemical poisoning.
[0003] Any conclusion drawn from current genotyping was limited because heterozygous (*A/0) and homozygous (*A/A) samples could yet not be discriminated. Phenotypically suggested high- and intermediate conjugators remained genotypically unexplained. The classification of all three genotypes has so far been hampered by the elucidation of the correct molecular mechanism of the GSTT1 deletion.
[0004] Thus, it is the object of this invention to provide a method for detecting the presence of at least one single allele of this deletion mutant.
[0005] This problem is solved by a method for detecting the presence of at least one single allele of a deletion mutant, wherein a PCR is performed with two primers, of which one stems from the sequence upstream of the deletion area, and the other stems from the sequence downstream of the deletion area, wherein the production of the corresponding DNA fragment in a PCR is checked.
[0006] It is preferred to use this invention for detecting the presence of at least one GSTT1*0 allele, wherein a combination of one primer form the enclosed sequence 1 and one primer from the enclosed sequence 2 is used and specific DNA fragments for the GSTT1*0 allele are obtained by PCR.
[0007] Thereby, using the following primers showed very good results:

CAG TTG TGA GCC ACC GTA CCC

CGA TAG TTG CTG GCC CCC TC

[0008] A special purpose of this invention is to use the invention in a procedure for diagnostic testing of patients to check whether they are susceptible to toxins or resistant to certain therapeutic agents or belonging to risk groups, wherein

- blood samples from the patients are obtained and genomic DNA is prepared from these blood samples
- a PCR-Mapping of the obtained DNA is performed using a combination of one primer from the enclosed sequence 1 and one primer from the enclosed sequence 2 and
- it is analysed whether corresponding DNA-fragments have been produced by the PCR.

[0009] In a preferred embodiment, there is an additional PCR mapping of the obtained DNA using a primer pair from within the GSTT1 gene and it is analysed whether PCR fragments of the primers according to claim 3 and/or PCR fragments of the primers from within the GSTT1 gene have been produced. In this way, all possible allele combinations (GSTT1*0/0, GSTT1*A/0 and GSTT1*A/A) can be detected.
[0010] It is preferred to use this GSTT1-genotyping assay to predict the risk for UV mediated skin damage and/or the genetic risk for skin cancer and/or the genetic risk for cancers that are associated with oxidative stress and/or damage.
[0011] In the following, the invention is explained in detail with reference to the enclosed figures and tables, wherein

Figure 1 shows the structure of the GSTT1 gene region and mapping of the deletion and the genomic organisation of GSTT1 (*A allele).

Figure 2 shows the mapping of the deletion and primer localization as well as selective primer combinations and corresponding PCR fragments for mapping of the deletion:

Primer Combinations	lane 1 and 2	GST-TF13/TRF13,

(continued)

	lane 3 and 4	GST-TF12/TRF12,
	lane 5 and 6	GST-TR11/TFR11,
	lane 7 and 8	GST-TR13/GST-TRF13;

Figure 3 shows the differentiation of GSTT1 genotypes by PCR assays:

a) Method according to the invention: a 1,5 kb fragment defines the *0/0 genotype, a 1,5 kb and 466 bp fragment indicate *A/O and a 466 bp fragment *A/A.

b) Method according to the state of the art: no fragment defines the *0/0 genotype, a 459 bp fragment indicates *A/0 or *A/A;

wherein lanes 1-3 represent samples from completely deleted (*0/0) individuals, lanes 4-6 from heterozygous (*A/0) and lanes 7-9 from homozygous *A individuals (*A/A), a 100 bp ladder (M) was used; identical samples were investigated;

Figure 4 shows the sequence and the mechanism of the GSTT1 deletion:
The schematic representation of the recombination event above and the sequence of the recombinant fragment;

Figure 5 shows the frequency distribution of GSTT1 conjugation activity in 130 samples; and

Figure 6 shows the mean UV skin sensivity by minimal erythema dose according to GSTT1 genotype in 60 healthy volunteers.

Table 1 shows the primers for the characterization of the GSTT1 deletion locus and diagnostic PCR;

Table 2 shows the GSTT1 allele distribution and phenotype correlation;

Table 3 shows the PCR fragments for GSTT1 genotyping; and

Table 4 shows the skin sensitivity to UV irradiation dependent on GSTT1 genotype.

[0012] The invention characterizes the structure and mechanism of the GSTT1 deletion by PCR mapping and sequencing: a 54251 bp fragment carrying the GSTT1 gene was deleted from the functional allele by a homoglogous recombination event. The deletion breakpoints are concealed within a 403 bp region on the null allele.

[0013] Based on this data a PCR assay using primer pairs (CAGTTGTGAGCCACCGTACCC, CGATAGTTGCTGGCCCCCTC) and (CCAGCTCACCGGATCATGGCCAG, CCTTCCTTACTGGTCCTCACATCTC) for GSTT1*0 and GSTT1*A, respectively, has been established according to the invention, that revealed all three GSTT1 genotypes (GSTT1*0/0, GSTT1*A/A, and GSTT1*A/0).
Furthermore, a Mendelian intermediary inheritance was proved by correlating the GSTT1 genotype with the enzyme activity using the substrate dichloromethane. Samples with two active alleles (GSTT1*A/A) expressed a statistically significant higher enzymatic activity compared to those with one null allele ($p<0.0001$, ANOVA).

[0014] This improved method can be introduced into routine genotyping as a new diagnostic tool and will help to elucidate the clinical relevance of this gene.

[0015] Glutathione S-transferase theta enzyme activity involved in the metabolism of toxic compounds is absent in approximately 20 % of Caucasians due to a homozygous deletion of *GSTT1* (**0/0*). Because the exact manner of the *GSTT1* deletion was unknown, current genotyping of *GSTT1* was limited to detect the presence vs complete absence of the gene by a *GSTT1*-specific PCR. Thus, heterozygous (**A/0*) and homozygous (**A/A*) samples could not be discriminated. The invention characterizes the boundaries of the deletion of the human glutathione *S*-transferase theta *(GSTT1)* gene: PCR mapping and sequencing revealed a 54251 bp fragment including *GSTT1* to be deleted from chromosome 22, most likely by a homologous recombination event between two highly homologous sequence stretches that flank *GSTT1*. Based on the knowledge of the *GSTT1*0* region, a PCR assay was devised for unambiguous discrimination of homozygously deleted (**0/0*), heterozygously (**A/0*) and homozygously *GSTT1* carrying (**A/A*) individuals. Genotyping of 180 samples of a Caucasian population revealed that the deletion consists of one defined allele, whose distribution in the population fits the Hardy-Weinberg equilibrium with observed 20 % **0/0*, 46 % **A/0* and 34

% *A/A individuals. The number of *GSTT1*A* alleles detected by this procedure correlated highly significant with the enzyme activity in erythrocytes. Genotype-phenotype comparisons proved a codominant type of inheritance by a gene-dose effect: samples with two active alleles expressed a statistically significant higher enzymatic activity compared to those with one null allele (p<0.0001, ANOVA).

[0016] Glutathione S-transferases (GSTs), a multi gene family of enzymes comprising several classes (class alpha, mu, pi, theta, and zeta), are expressed in many tissues, including liver, lung, heart, intestine, erythrocytes, and lymphocytes (Hayes et al., 1995). GSTs regulate the conjugation of toxic compounds to excretable hydrophilic metabolites. Because of that, their activity may affect individual susceptibility to environmental toxins, carcinogens, cancer, and other diseases (Strange 1999). The glutathione S-transferase theta (*GSTT1*) gene, and its corresponding enzyme activity is lacking in about 20 % of Caucasians (Brockmöller et *al.*, 1996). However, even within the Caucasian population, this frequency differs with respect to ethnicity (Nelson et *al.*, 1995). A non-functional *GSTT1* allele (*GSTT1*0*) is the result of a partial or complete deletion of the gene, the enzyme is completely absent in homozygots (*GSTT1*0/0*) (Pemble *et al.*, 1994). Many chemicals, such as halogenated alkanes and epoxides whose use is widely spread in industry, are substrates for GSTT1 and thus their toxicity can be modulated by GSTT1. Interestingly, glutathione conjugation may cause detoxification as well as toxification. For instance, the conjugation of dichloromethane yields the toxic metabolite formaldehyde (Hallier et al., 1994) and the mutagenicity of several halogenated alkanes was enhanced in a GSTT1-expressing model system (Their *et al.*, 1996). Thus, *GSTT1* polymorphism may determine individual susceptibility towards toxic compounds. For example, of two workers that were accidentally exposed to methyl bromide, the GSTT1 conjugator suffered severe poisoning while the deficient developed only mild neurotoxic symptoms (Garnier *et al.*, 1996). Since glutathione conjugation may provide a step in elimination of substances which are toxic *per se*, GSTT1 activity can also act protective (Ketterer *et al.*, 1993). This explains that GSTT1 protected human lymphocytes from DNA and chromosomal damage after exposure to several halomethanes (Wiencke *et al.*, 1995; Hallier *et al.*, 1993). Consequently, GSTT1 has been investigated as risk factor in epidemiological studies. The deletion conferred an increased risk in myelodysplastic syndrome (Chen *et al.*, 1996) and some studies have suggested a correlation with susceptibility of the skin to UV-irradiation (Kerb *et al.*, 1997). Although substantial data on epidemiological associations between GSTT1 deficiency and cancer exist, the results are conflicting, which might be partly due to limitations of the currently used genotyping procedures for *GSTT1.* Using biochemical analyses, three groups, high-, intermediate-, and non-conjugators, can be discriminated (Hallier et al., 1990). This may suggest a Mendelian intermediary inheritance (Wiebel et al., 1999), but so far the genetic background of intermediate and high conjugators and a gene-dose effect could not be unambiguously established. The currently used genetic assay for GSTT1 deficiency is a gene-specific PCR fragment that *is present in conjugators, and absent in GSTT1*0/0. The frag*ment is therefore diagnostic for the presence of at least one functional allele (*GSTT1*A*) and a differentiation between homo- and heterozygous carriers of *GSTT1*A* is not possible, according to the state of the art.

[0017] This invention shows the characterization of the *GSTT1* deletion, probably the result of a recombination event between two highly homologous regions that flank the *GSTT1* gene. Utilizing the sequence of the *GSTT1*0* recombination region, a PCR assay was devised that permits not only the unequivocal determination of homozygously deleted (*0/0) but also the discrimination of the heterozygously (*A/0) from the homozygously active (*A/A) individuals. The three *GSTT1* genotypes detected by this procedure correlated highly significant with enzyme activity in erythrocytes. The trimodular distribution of phenotypes with high-, intermediate-, and null activity in homo- and heterozygotes for the *A allele and *0/0 homozygotes, respectively, indicates a gene-dose effect.

[0018] For initial determination and characterization of the *GSTT1* deletion, samples of caucasian volunteers from the Dr. Margarete Fischer-Bosch-Institute of Clinical Pharmacology in Stuttgart, and from the Institute of Clinical Pharmacology at the University Medical Center, Charité in Berlin have been used. Samples were obtained under consideration of all ethical and legal requirements. Genomic DNA was prepared from blood using the Qiagen (QiaAmp) kits on a Qiagen 9604 robot. For geno-phenotype correlations, phenotyped subjects have been used (n=130, male, mean age 30.7 years, ranging from 22 to 49 years) which were part of a previous study (Bruhn *et al.* 1998), DNA was obtained from these samples using phenol/chloroform extraction.

[0019] Determination of formaldehyde production rate (pmol HCHO/min/µl) from 31, 62, and 124 mM dichloromethane in hemolysate was used as a measure for GSTT1 activity (Bruhn et *al.*, 1998).

[0020] NCBI database entries Z84718.1 and AP000351.2 (Genbank) contain GSTT1 sequences in annotated form (Z84718.1) or as raw data files, respectively. DNA sequence comparisons, alignments and the construction of composite files from raw data sequence files were performed using the programs FASTA and BLAST at the NCBI server.

[0021] Specific oligonucleotide primers for PCR of *GSTT1* gene fragments from genomic DNA were derived (Table 1). Sequences of purified PCR fragments were obtained by automated DNA sequencing on ABI 377 (gel) or ABI 3700 (capillary) sequencers using BigDye Terminator cycle sequencing reactions (PE Biosystems). Amplification of fragments less than 2kb was performed in 25µl volume: 100 ng DNA template added to buffer containing 1.5 mM $MgCl_2$, 200 µM dNTPs, 0.2 mM each primer and 1 U HotStarTaq polymerase (all reagents Qiagen, Hilden, Germany) . PCR was carried out in a Perkin Elmer GeneAmp System 9700 with an initial denaturation of 15 min at 95°C followed by

30 cycles of 94°C for 30 s, 30 s annealing and 60 s of extension at 72°C. Final extension was carried out for 7 min at 72°C. For longer amplicons 50µl PCR reactions contain 200 ng of genomic DNA, reaction buffer 3, 500 µM dNTPs, 2.6 U Expand Taq-System (Roche, Basel, Switzerland) and 0.3 mM primers (Metabion, Munich, Germany). Samples were incubated at 92°C for 2 min, followed by 35 cycles at 92°C for 10 s, 45 s annealing at 68°C for each kb per min extension time. The extension time of each cycle was increased by 20 s for the last 25 cycles. 10 min final extension at 68°C were applied.

[0022] The human *GSTT1* gene is located on chromosome 22q11.2 which has recently been completely sequenced in the course of the human genome sequencing project (Dunham *et al.*, 1999); prior to that, partial chromosome sequences were available in public databases from the Sanger Center. A 76799 bp DNA sequence of a BAC clone (gb: Z84718.1) contains the *GSTT1* and the *GSTT2* gene. Homology searches in unnotated raw sequences revealed one additional *GSTT1*-containing clone, AP000351.2 (118999 bp) consisting only of preliminary BAC sequences which are not assembled to a defined linear gene. A defined sequence file that contains *GSTT1* and the flanking regions, which extends the annotated *GSTT1* gene region of clone Z84718.1 was constructed by homology alignments using FASTA and BLAST at the NCBI server. Due to the high homology of parts of the sequences, the stringency of the alignments was set higher than default and the correctness of the assembled sequence was confirmed by visual inspection. The composition and prominent features of the *GSTT1* gene region are shown in figure 1: *GSTT1* and the homologous *GSTT2* gene (55 % protein homology, Tan *et* al., 1995) are separated by 49741 bp. In addition to many repetitive elements, *GSTT1* is flanked by 18-kb regions which are more than 90 % homologous (defined in the **A* i.e. non-deleted allele, as homology region HA5 upstream and HA3 downstream of *GSTT1*).

[0023] Although the detailed site of the *GSTT1* deletion was unknown, the homozygous null allele could be diagnosed by the absence of a PCR fragment that is specifically amplified from the *GSTT1* coding region (Pemble *et al.*, 1994). The deletion removes *GSTT1* but not *GSTT2* (Tan *et al.*, 1995). Therefore, one breakpoint of the deletion is positioned between *GSTT1* and *GSTT2* and the other must be downstream of *GSTT1* (Fig. 1). To map the *GSTT1* deletion we determined the presence or absence of specific sequences upstream and downstream of *GSTT1* by PCR. Ten samples of the genotype *GSTT1*0/0*, and ten samples with at least one *GSTT1*A* allele were preselected (see Fig. 3a). Primer sets for specific amplification of fragments up- and downstream of *GSTT1* were generated. This required extensive optimization considering the highly homologous flanking regions of *GSTT1*. Fragments that could be amplified from both, *GSTT1*0/0* and samples containing at least one *A allele (**A*) were regarded to be outside the deletion, whereas fragments that could exclusively be amplified from **A* samples, but not from *0/0 contain the region which is deleted. Figure 2 shows results of this mapping procedure. Primer combinations that bind upstream from position 50191, and downstream from position 110007 of the sequence file can be obtained from all samples. Fragments closer to *GSTT1*, downstream position 53494 and upstream position 105675 cannot be amplified from **0/0* samples. Therefore, the boundaries of the deletion must be localized within a region between position 50192 to 53493 upstream and 105676 to 110006 downstream of *GSTT1*.

[0024] To home in on the exact positions of the deletion, we applied long range PCR has been applied to span the deletion in **0/0* samples. Various sets of PCR primers were selected close to the deletion boundaries as defined by PCR-mapping. In *GSTT1*A* samples, the 5'and 3'primers were separated by more than 60 kb, in **0/0* samples the distance between these primers was reduced by the size of the deletion. Utilizing different primer combinations, reproducibly deletion-spanning PCR fragments of 10065 bp, 3187 bp and of 1460 bp have been generated (Fig. 3, Table 3 for primer positions). The 10 kb fragment was sequenced to characterize the deletion region. The comparison of this null allele sequence with the *GSTT1*A* allele revealed the boundaries of the deletion (Fig. 4): it is flanked upstream and downstream by sequences that are part of the highly homologous HA5 and HA3 regions. In the **A* allele, these regions flank *GSTT1*. In **0*, the deletion generates a fusion sequence (H0) which differs from HA5 and HA3 by only a few nucleotide deviations as shown in Figure 4. Using these deviations as "markers", for identification of the HA5 or HA3 portions of H0, the region where the deletion had happened could be narrowed down to a 403 bp sequence stretch. This sequence is identical in HA5 and HA3. These data support the assumption that the mechanism which generated the deletion is homologous recombination between the regions HA5 and HA3, which removes *GSTT1* and generates H0.

[0025] The method according to the state of the art to analyze *GSTT1* includes a critical negative test output: lack of a PCR signal defines **0/0* samples, whereas generation of the fragment detects the presence of at least one *GSTT1*A* allele (**A/A* or **A/0*). In addition to problems associated with negative test readouts (e.g. false results due to test failure may be misinterpreted as **0/0*), another drawback of that method is that homozygous (**A/A*) and heterozygous (**A/0*) samples cannot be distinguished. Utilizing the molecular composition of the deletion, the invention devises a new genotyping protocol that allows not only a positive detection of the deletion allele, but also permits the unambiguous discrimination of all *GSTT1* genotypes (**A/A*, **A/0*, and **0/0*). The procedure generates deletion-spanning PCR fragments, which are combined with fragments that indicate the presence of *GSTT1*. Various PCR assays were evaluated using *GSTT1* fragments in combination with deletion spanning fragments of sizes between 10065 and 1460 bp (table 3). Among these, one assay that had been established was found to be "robust" and allowed a reproducible simulta-

neous discrimination of all genotypes. The 1460 bp deletion-specific PCR fragment was combined with a 466 bp fragment that detected *GSTT1*A*. Figure 3 shows the results of this assay applied to known **0/0* samples and **A/?* samples: all samples that had previously been genotyped homozygous for the deletion by the standard method confirmed the **0/0* genotype with a positive readout of 1460 bp. The genotype *GSTT1*A/A* is diagnosed by the single 466 bp fragment and can be differentiated from heterozygous individuals who are characterized by the presence of both fragments. Testing more than 50 *GSTT1*0/0* samples, no discrepancies were detected between the methods according to the state of the art and according to the invention.

[0026] The *GSTT1*0/0* genotype correlates with the non conjugator phenotype. To evaluate whether intermediate and high conjugators are caused by **A/0* and **A/A* genotypes, 130 samples whose GSTT1 activity in blood had been determined have been genotyped. Figure 5 shows that the three *GSTT1* genotypes could be assigned to distinct phenotypes: enzyme deficiency in *GSTT1*0/0* samples, intermediate activity in **A/0* samples, and high activity in **A/A* samples has been observed. The correlation of genotype and phenotype is statistically highly significant, $p<0.0001$ for all group comparisons (ANOVA with Bonferroni/Dunn correction for multiple testing). The allelic frequencies were in agreement with Hardy-Weinberg's law, the difference between observed and expected results (calculation based on the frequency of **0/0*) was not significant (Table 2).

[0027] *Characterization and mechanism of the GSTT1 deletion: The invention allows to* characterize the structure and mechanism of the *GSTT1* deletion and identify two 18 kb homology regions flanking *GSTT1* which are involved in the deletion (most likely crossing over) event that produced the **0* allele. Extensive sequence identity between both repeat regions in the **A* allele, and between these repeats and the corresponding region in the deletion allele allowed to define the deletion boundaries within a 403 bp region. Gene deletion by homologous unequal crossing over has been described in other detoxification enzymes, in cytochrome P450 2D6 and glutathione *S*-transferase M1 (Steen *et al.*, 1995; Xu *et al.*, 1998; Kerb *et al.*, 1999). Like in *GSTM1*, the *GSTT1* deletion has a high frequency in the Caucasian population. Does this deletion consist of one defined null allele or are there various deletions with the loss of *GSTT1* as the common denominator ? Since the assay showed the deletion allele as "measurable" PCR fragment, any variations in the size of the deletion indicative of multiple deletion alleles would have been detectable. In more than 150 **0* allele harboring samples that have been analyzed, the "deletion fragment" showed the same size of 1460 bp, suggesting that all *GSTT1* deficiencies are caused by one allele.

[0028] Improved genotyping assay and allele distribution in Caucasians: So far, genotyping could detect the absence of GSTT1, but provided neither information about the boundaries of the deletion nor about the precise genotype. In spite of the extreme homology, a few single nucleotide variations specific for the recombinant region allow to create an assay for the detection of the inactive allele by presence of a PCR-fragment. A single PCR assay that detects this deletion-spanning PCR-fragment, combined with a fragment that indicates the presence of GSTT1, allows the unambiguous discrimination of all genotypes. Using the assay, the allele distribution was analyzed in Caucasian individuals and found to be 34% homozygous *A/A, 46% heterozygous, and 20% *0/0. This frequency fits to the distribution that would be expected on the basis of Hardy-Weinberg equilibrium (Table 2).

[0029] GSTT1 as risk factor in cancer: A number of epidemiological studies have been published on the medical importance of GSTT1 (Strange and Fryer, 1999). GSTT1*0/0 was found to be associated with brain cancer (Kelsey et al., 1997, Elexpuru Camiruaga et al., 1995), head- and neck cancer (Cheng *et al.*, 1999), lung cancer in Hispanic- and African Americans (Kelsey *et al.*, 1997). However, results were often ambiguous (Duncan *et al.*, 1995, Heagerty *et al.*, 1996) or gave conflicting results in bladder cancer (Kempkes *et al.*, 1996, Brockmöller et *al.*, 1996) and colorectal cancer (Clapper and Szarka, 1998; Zhang *et al.*, 1999, Chenevix-Trench *et al.*, 1995; Katoh et al., 1995; Gertig *et al.*, 1998). In all these studies only a comparison of the null genotype with an active genotype was done. The difference between heterozygous and homozygous active individuals has not yet been elucidated, but determining both, could improve the statistical power in epidemiological studies.

[0030] *Genotype-Phenotype correlation:* Phenotypic data have indicated the presence of intermediate conjugators displaying only half the activity of high conjugators (Warholm *et al.*, 1995). These observations, and a family study that analyzed *GSTT1* by semiquantitative PCR (Wiebel *et al.*, 1999), suggest a gene-dosage effect on GSTT1 activity. In this, it has unambiguously been proven the intermediate Mendelian type of inheritance of *GSTT1* for the first time. The enzyme activity of GSTT1 correlated highly significant with the number of functional alleles and phenotypically classified intermediate- and high conjugators were genotypically detected hetero-(GSTT**A/0*) and homozygous (**A/A*), respectively. In only 9 among a total of 130 samples the genotype did not correlate well with the phenotype. Three intermediate conjugators had two active alleles and 6 samples with high enzyme activity displayed unexpectedly only one active allele. Since the enzymatic activity of all discrepant individuals was close to the antimode and the enzyme assay had a CV of 7 %, differences are most likely the result of biological variability. With codominant inheritance, each allele confers a measurable, yet variable component to the phenotype resulting in a wide range of enzymatic activities from a distinct genotype and overlapping activities between homo- and heterozygotes. Furthermore, GSTT1 genotype-phenotype discrepancies can be modulated by exposure to inducers or inhibitors, whereas the genotype remains constant. Two other subjects attracted our attention because their extraordinary high conjugation activity was 2-fold

higher than the mean of homozygous conjugators (68 pmol/min/µl versus 32 pmol/min/µl, Fig. 5). These subjects displayed the *A/A genotype in our assay. One possible explanation could be a gene duplication or amplification of *GSTT1*. Members of the GST multigene family have been evolutionary derived from a Theta-class gene duplication (Pemble and Taylor, 1992), and a duplicated class M1 gene that causes ultrarapid enzyme activity has already been described (McLellan *et al.*, 1997). Thus, it is feasible that rare (2 of 130) ultrahigh GSTT1 activity may be caused by additionally amplified gene copies.

[0031] The identification of *GSTT1* genotypes with a procedure that unambiguously discriminates *0/0, *A/0 and *A/A alleles predicts highly significant the phenotype and will allow an accurate assessment of health risk from halogenated alkanes or pesticides (Bruning *et al.*, 1997; Au *et al.*, 1999; El-Masri *et al.*, 1999). It also provides a useful approach for the evaluation of the importance of GSTT1 as risk factor for various diseases.

[0032] This invention is especially suitable to check whether an individual has a genetic risk for UV mediated skin damage and/or skin cancer and/or cancers that are associated with oxidative stress and/or damage.

[0033] Ultraviolet (UV) irradiation by sun exposure and family history are risk factors for the development of cutaneous melanoma. Inherited susceptibility to this type of skin cancer could therefore result from genetic factors that affect the capacity of cells to prevent UV-induced DNA lesions. UV light mediates the formation of radical oxygen species (ROS) such as hydroxyl and superoxide radicals, hydrogen peroxide, and single oxygens. These molecules comprise "oxidative stress" and damage cellular proteins, lipids, and DNA. Oxidative stress can cause inflammation, mutations, and genotoxicity. The skin is equipped with a defense system against oxidative stress (Vessey, 1993). Glutathione S-transferases (GSTs) contribute to this protection either by direct inactivation of peroxidized lipids and DNA (Berhane et al., 1994; Ketterer and Meyer, 1989; Tan et al., 1988), or by detoxification of xenobiotics, which can serve as cofactors of radical formation. Our improved assay system to detect GSTT1 deficiencies and heterozygotes shows that GST genotypes affect the susceptibility of individuals to oxidative or chemical stress. Figure 6 shows the results of a panel comparison of two groups of genotypically characterized GSTT1 deficient, homozygous and heterozygous active subjects in respect to sunlight (UV) sensitivity. The GSTT1 genotyping was performed with the assay according to the invention that is described above. Healthy subjects (54 male, 6 female, 18 to 48 (mean 27.6) years old and of German Caucasian origin were selected for the panel comparison study. The constitutional skin types were assigned from tanning and burning histories using the Fitzpatrick's Classification (Fitzpatrick et al., 1987) and the study was performed during the winter months. Reactivity to UV light was determined in eight skin fields (1 x 0.6 cm) on non-UV exposed buttock skin by increasing doses of simulated sunlight with 20% dose increments (Wucherpfennig, 1931). Before each irradiation, UV intensity of the radiation source (dermalight 2001‰ equipped with an h2 filter, Dr. Höhnle, Munich, Germany) was calibrated to 1.33 mW/cm^2 at 280-315 nm, by use of a UVA/B Meter (Dr. Höhnle). UV dose [J/cm2) was calculated by intensity [mW/cm^2] x time [sec] / 1000. Dose variations, from 0.07 J/cm^2 to 0.34 J/cm^2, were achieved by irradiation time. Erythema reactions were scored visually 20 hours post-exposure, independently by two examiners. All skin reactions were photographically documented. The irradiation dose of the first field with a barely perceptible erythema determined the minimal erythema dose (MED). The software package for statistical analyses SPSS 10.0 was applied to evaluate genotype-phenotype correlation and statistical significance (SPSS Inc., Chicago, USA). The dependency of UV sensitivity from genotype was tested with ANCOVA to control for constitutional skin type as confounding variable. Adjustment for multiple testing was done according to Bonferroni/Dunn.

The results of the panel comparison study showed a clear correlation of *GSTT1*-genotype and UV sensitivity of the skin: The *GSTT1*-deficient group has a higher inflammatory response after exposure to UV irradiation compared to the group with GSTT1 activity. Subjects homozygous for the *GSTT1* deletion mutation required a statistically significant lower UV dose to barely perceptible erythema than those with one (*GSTT1**A/0*; $p=0.067$) or two (*GSTT1**A/A*; $p=0.032$) functionally active alleles. The erythema reaction did not decrease with the number of functional alleles and was equal in both *GSTT1**A/0* and **A/A* subjects. Among the 5 most UV-sensitive subjects (MED $\leq$ 0.10 J/cm^2) were 4 *GSTT1* deficient and the two subjects with the lowest inflammatory response (MED $\geq$ 0.29) were both of enzyme-expressing genotype.

GSTT1 and GSTM1 are expressed in the skin and deficiencies in these enzymes by gene deletions impairs the capacity of cells to detoxify specific substrates, which include molecules that are generated by oxidative damage. The modification of molecules with reactive oxygens as substrate of GSTs provides one link between GSTs enzyme activity and protection against UV radiation-induced cutaneous damage. GST deficiencies result in increased susceptibility of cells to the consequences of ROS attack, such as inflammation or cancerogenesis (Fahey and Sundquist, 1991). UV irradiation by sun exposure and family history are risk factors for the development of skin cancer, particularly cutaneous melanoma. The fact that the *GSTT1* and, to a lesser degree the *GSTM1* genotype identifies individuals with increased UVsunlight-sensitivity, suggests *GSTT1* and *-M1* genotype variations to be among the genetic components that result in the inherited susceptibility or predisposition to skin cancer.

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Claims

1. Method for detecting the presence of at least one single allele of a deletion mutant, **characterized in that** a PCR is performed with two primers, of which one stems from the sequence upstream of the deletion area, and the other stems from the sequence downstream of the deletion area, wherein the production of the corresponding DNA-fragment in the PCR is checked.

2. PCR-Assay for detecting the presence of at least one GSTT1*0 allele characterized by using a combination of one primer from the enclosed sequence 1 and one primer from the enclosed sequence 2 and obtaining specific DNA-fragments for this allele by PCR.

3. Assay according to claim 1, characterized by using the combination of the primers CAG TTG TGA GCC ACC GTA CCC and CGA TAG TTG CTG GCC CCC TC

4. Procedure for diagnostic testing of individuals to check whether they are susceptible to toxins or resistant to certain therapeutic agents or belonging to risk groups characterized by

   - obtaining blood samples from the individuals and preparing genomic DNA from these blood samples

   - PCR mapping of the obtained DNA using a combination of one primer from the enclosed sequence 1 and one primer from the enclosed sequence 2 and

   - analysing whether corresponding DNA fragments have been produced by PCR.

5. Procedure according to claim 4, characterized by

   - further PCR mapping of the obtained DNA using a primer pair from within the GSTT1 gene and

   - analysing whether PCR fragments of the primers according to claim 3 and/or PCR fragments of the primers from within the GSTT1 gene have been produced.

6. Procedure according to claim 4 or 5, **characterized in that** the risk for UV-mediated skin damage and/or the genetic risk for skin cancer and/or the genetic risk for cancers that are associated with oxidative stress and/or damage is predicted according to the results of the PCR mapping.

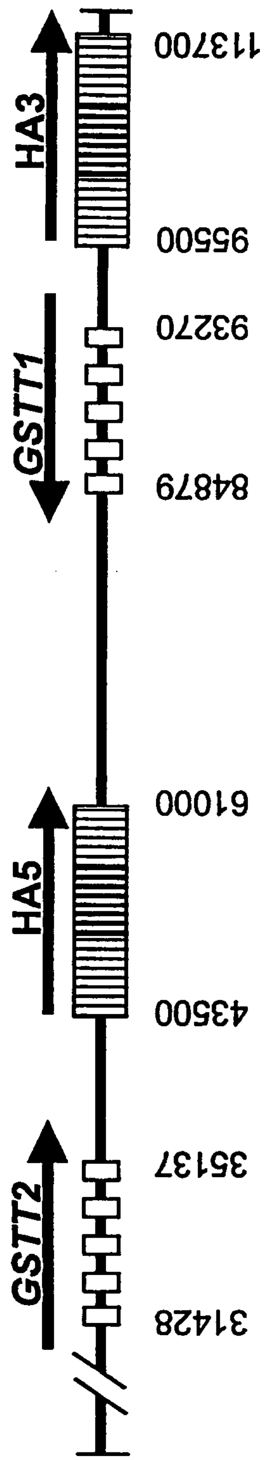
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Fig. 1

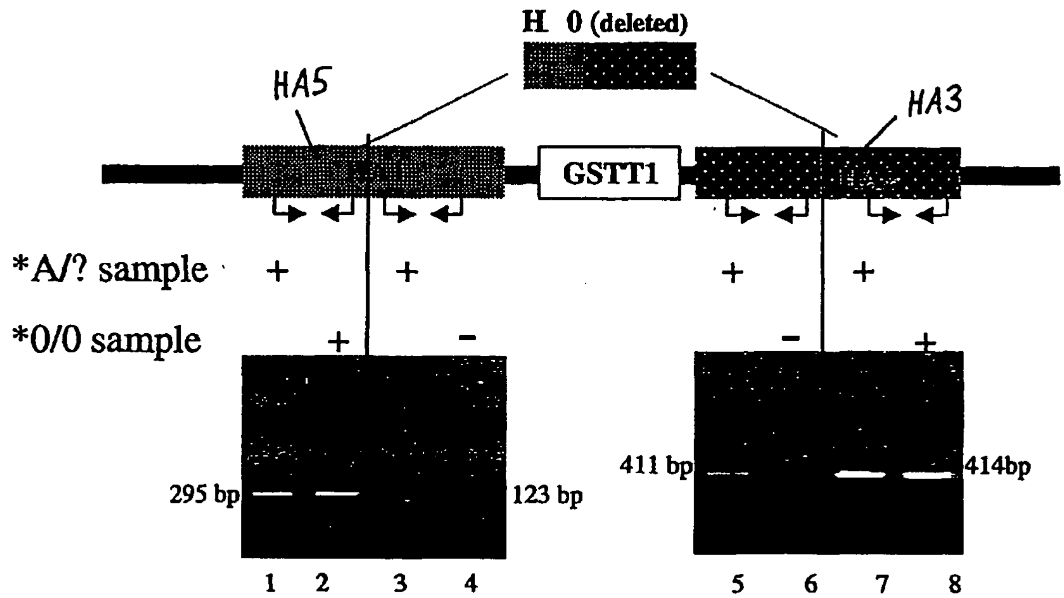
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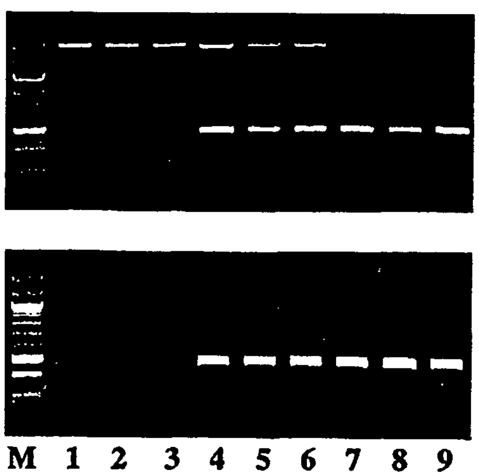
Fig. 2.

a

b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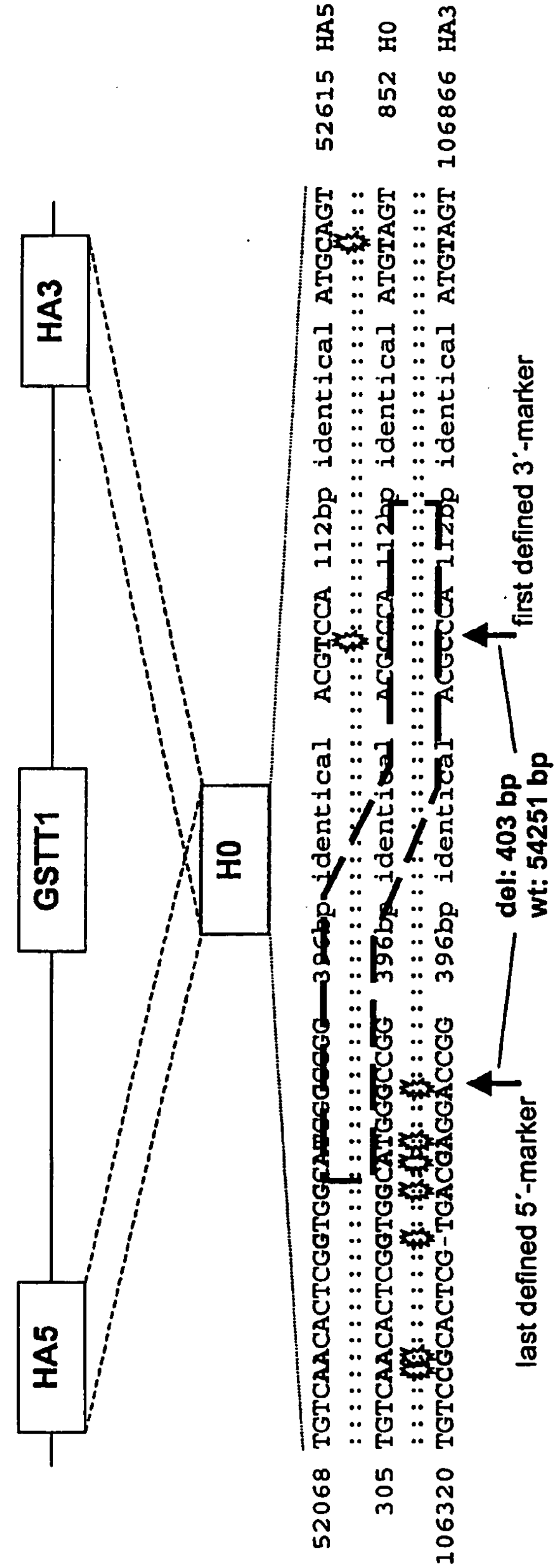
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Fig. 4

Fig. 5

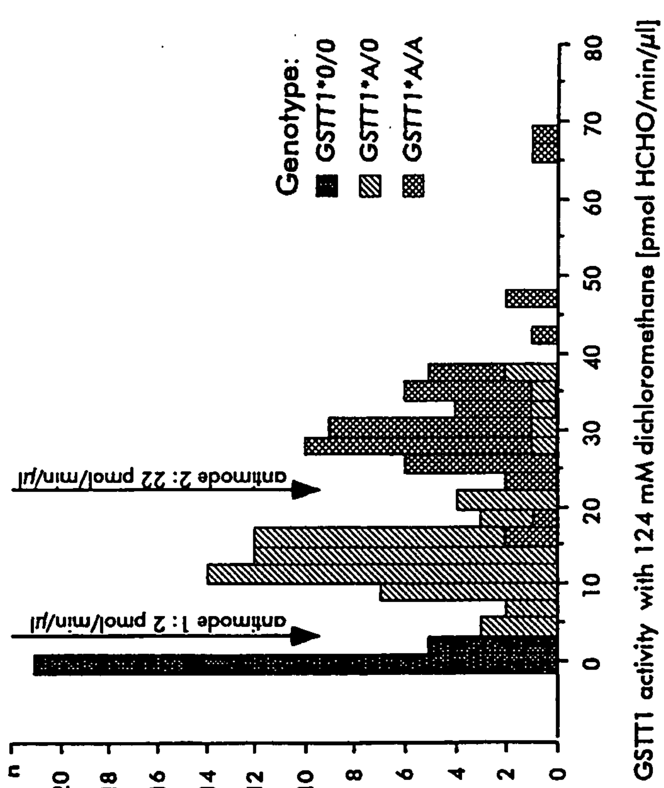
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Fig. 6

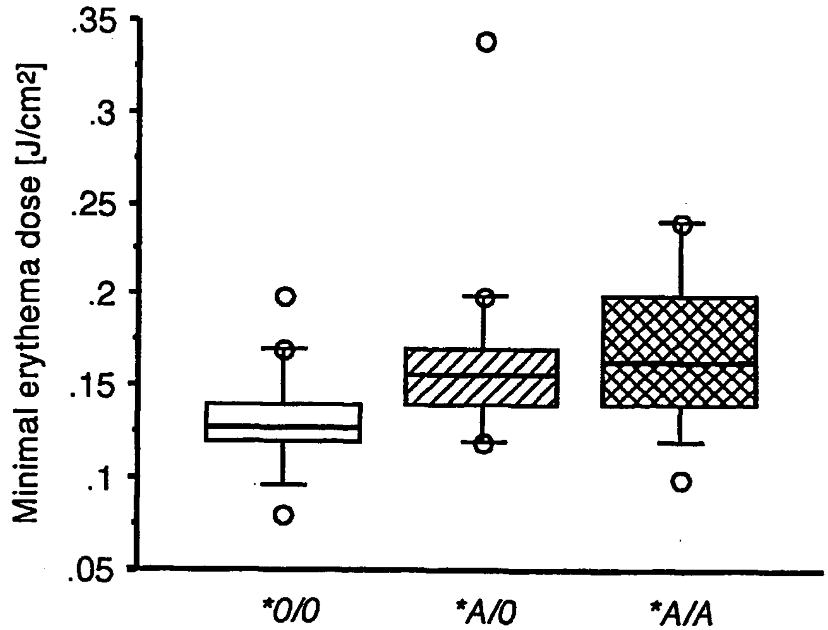

Table 1: Primers for the characterization of the GSTT1 deletion locus and diagnostic PCR

Name	Primer sequences [5'-...-3']	Annealing [°C]	Primer positions 5'	3'
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GST-TR	TCA CCG GAT CAT GGC CAG CA		85462*	85481*
	PCR mapping primers			
GST-TF13	CCC TCA CTC AGG GTT AGT GG	63	110007*	110026*
GST-TRF13	GAT GCC ACG CGG CTT GTA GG		110301*	110282*
GST-TF12	GAT TGG TGG AAG GTG CCG GG	63	105553*	105576*
GST-TRF12	CGT GTC TCT ACT TCA AAT TCC ATG		105675*	105652*
GST-TFR11	TAA GAT ACC TCA TAA AAT TAA CAG	59	53904*	53881*
GST-TR11	GGC AGA ATG GAT AGT GGG GAG		53494*	53514*
GST-TFR13	GCA AGA AGA CCA GTG ACT GAG G	63	50191*	50170*
GST-TR13	CTG CTC TTC TTC AGC AAC TCA G		49778*	49800*
	10065 bp *0 fragment primers			
GST-TRF13	GAT GCC ACG CGG CTT GTA GG	65	110301*	110282*
GST-TR12	CTT TTT CTG CAC CAA ACG CAT TG		45986*	46008*
	3187 bp *0 fragment primers			
GST-TRF13.2	CAG CCA AGA AGT TCT GAG TCT TG	65	108037*	108015*
GST-TR9n	ATA TCA GCC AGA GAT CTC TGG G		50600*	50621*
	Sequencing primers			
GST-TRF13.3	GCA TCC CAA TTC AAC ACG TGT TG	62	107075*	107053*
GSTT-F.1000	CTT CTC AGC TGA AAC TTC CTC		51440*	51460*
	GSTT1 deletion assay primers			
GT*Af	CCA GCT CAC CGG ATC ATG GCC AG	70	85457*	85479*
GT*Ar	CCT TCC TTA CTG GTC CTC ACA TCT C		85922*	85898*
GT*0f	CAG TTG TGA GCC ACC GTA CCC		52069*/6084**	52089*/6114**
GT*0r	CGA TAG TTG CTG GCC CCC TC		107779*/7543**	107760*/7524**

* : according to AP000351.2

**: according to *GSTT1 *0*

Table 2: *GSTT1* allele distribution and phenotype correlation

Genotype	**A/A*	**A/0*	**0/0*
N	44	60	26
% observed	33.8	46.2	20.0
% expected[a]	30.6[b]	49.4[b]	20.0[b]
Mean (SD) enzyme activity	32.1(10.2)[c]	15.0(7.4)[c]	3.3(0.9)[c]

[a]based on **0/0*, according to Hardy-Weinberg
[b]$\chi^2 = 0.23$
[c] $p<0.0001$, ANOVA with Bonferroni/Dunn correction for multiple testing

Table 3: PCR-fragments for *GSTT1* genotyping.

Sequence	Position	Size [bp]	Specificity	Comment
GATGCCACGCGGCTTGTAGG	45986 – 46008	10065	*GSTT1*0*	Long range PCR
CTTTTTCTGCACCAAACGCATTG	110301-110282			
ATATCAGCCAGAGATCTCTGGG	50600-50621	3187	*GSTT1*0*	Long range PCR
CAGCCAAGAAGTTCTGAGTCTTG	108015-108037			
CAGTTGTGAGCCACCGTACCC	52069-52089	1460	*GSTT1*0*	Standard PCR
CGATAGTTGCTGGCCCCCTC	107779-107760			
CCAGCTCACCGGATCATGGCCAG	85457-85479	466	*GSTT1*A*	Standard PCR
CCTTCCTTACTGGTCCTCACATCTC	85922-85898			

Table 4

	GST-Enzyme Activity	n	MED (J/cm^2)[a]		
			Mean	Range	SD
*GSTT1*A/A*	High	15	0.164	0.10-0.24	0.043
*GSTT1*A/0*	Intermediate	22	0.157	0.12-0.29	0.048
*GSTT1*0/0*	Deficient	23	0.129	0.08-0.20	0.027
Total		60	0.145	0.08-0.29	0.037

[a]Inflammatory reaction was detected as minimal erythema dose (MED) at 20 h after irradiation with UV

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Application Number
EP 00 10 3844

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The present search report has been drawn up for all claims

Place of search	Date of completion of the search	Examiner
THE HAGUE	25 August 2000	Knehr, M

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